

#7

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/703,253

DATE: 08/15/2001

TIME: 08:20:17

Input Set : A:\lex81usa SEQLIST.TXT

Output Set: N:\CRF3\08132001\I703253.raw

ENTERED

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4 <110> APPLICANT: Harras, Marie
 5 Donoho, Gregory
 6 Turner, C. Alexander Jr.
 7 Nehls, Michael
 8 Friedrich, Glenn
 9 Zambrowicz, Brian
 10 Sands, Arthur T.
 12 <120> TITLE OF INVENTION: Novel Human Transporter Proteins and
 13 Polynucleotides Encoding the Same
 16 <130> FILE REFERENCE: LEX-0081-USA
 18 <140> CURRENT APPLICATION NUMBER: US/09/703,253
 18 <141> CURRENT FILING DATE: 2000-10-31
 18 <150> PRIOR APPLICATION NUMBER: US 60/163,018
 19 <151> PRIOR FILING DATE: 1999-11-02
 21 <160> NUMBER OF SEQ ID NOS: 25
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1977
 27 <212> TYPE: DNA
 28 <213> ORGANISM: homo sapiens
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 32 cgtgtgacca gtgaagttct cacttgcatc aagctgatta aaatgtacac atgggagaaa 120
 33 ccatttgcaa aaatcattga agacctaaga aggaaggaaa ggaagctatt ggagaagtgc 180
 34 gggcttgctc agagcctgac aagtataacc ttgttcacat tccccacagt ggccacagcg 240
 35 gtctgggttc tcatccacac atccttaaag ctgaaactca cagcgtcaat ggccttcagc 300
 36 atgctggcct ccttgaatct ccttcggctg tcagtgttct ttgtgcctat tgcagtcaaa 360
 37 ggtctcacga attccaagtc tgcagtgatg aggttcaaga agtttttctt ccaggagagc 420
 38 cctgttttct atgtccagac attacaagac cccagcaaag ctctgggtctt tgaggaggcc 480
 39 accttgatcat ggcaacagac ctgtcccggg atcgtcaatg gggcactgga gctggagagg 540
 40 aacgggcatg cttctgaggg gatgaccagg cctagagatg ccctcggggc agaggaagaa 600
 41 gggaacagcc tgggcccaag gttgcacaag atcaacctgg tgggtgtccaa ggggatgatg 660
 42 ttaggggtct gcggcaacac ggggagtggg aagagcagcc tgttgtcagc catcctggag 720
 43 gagatgcact tgctcgaggg ctcgggtggg gtgcagggaa gcctggccta tgtccccag 780
 44 caggcctgga tcgtcagcgg gaacatcagg gagaacatcc tcatgggagg cgcatatgac 840
 45 aaggcccgat acctccaggt gctccactgc tgctccctga atcgggacct ggaacttctg 900
 46 ccctttggag acatgacaga gattggagag cggggcctca acctctctgg ggggcagaaa 960
 47 cagaggatca gcctggcccg cgccgtctat tccgaccgtc agatctacct gctggacgac 1020
 48 cccctgtctg ctgtggacgc ccacgtgggg aagcacattt ttgaggagtg cattaagaag 1080
 49 aactcaggg ggaagacggt cgtcctgggtg acccaccagc tgcagtactt agaattttgt 1140
 50 ggccagatca ttttgttgga aaatgggaaa atctgtgaaa atggaaactca cagtgaagta 1200
 51 atgcagaaaa aggggaaata tgcccaactt atccagaaga tgcacaagga agccacttcg 1260
 52 gacatgttgc aggacacagc aaagatagca gagaagccaa aggtagaaag tcaggctctg 1320
 53 gccacctccc tggaagagtc tctcaacgga aatgctgtgc cggagcatca gctcacacag 1380
 54 gaggaggaga tggaagaagg ctccttgagt tggagggtct accaccacta catccaggca 1440
 55 gctggagggtt acatggtctc ttgcataatt ttcttcttcg ttgtgctgat cgtcttctta 1500
 56 acgatcttca gcttctggtg gctgagctac tgggttgagc agggctcggg gaccaatagc 1560

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57 agccgagaga gcaatggaac catggcagac ctgggcaaca ttgcagacaa tcctcaactg 1620
58 tccttctacc agctggtgta cgggctcaac gccctgctcc tcattctgtgt gggggtctgc 1680
59 tcctcaggga ttttcaccaa ggtcacgagg aaggcatcca cggccctgca caacaagctc 1740
60 ttcaacaagg ttttcgctg ccccatgagt ttctttgaca ccatcccaat aggccggtt 1800
61 ttgaactgct tcgcaggga cttggaacag ctggaccagc tcttgcccat cttttcagag 1860
62 cagttcctgg tcctgtcctt aatggtgatc gccgtcctgt tgattgtcag tgtgctgtct 1920
63 ccatatatcc tgtaaatggg agccataatc atggttattt gcttcattta ttatatg 1977
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 659
67 <212> TYPE: PRT
68 <213> ORGANISM: homo sapiens
70 <400> SEQUENCE: 2
71 Met Thr Arg Met Ala Val Lys Ala Gln His His Thr Ser Glu Val Ser
72 1 5 10 15
73 Asp Gln Arg Ile Arg Val Thr Ser Glu Val Leu Thr Cys Ile Lys Leu
74 20 25 30
75 Ile Lys Met Tyr Thr Trp Glu Lys Pro Phe Ala Lys Ile Ile Glu Asp
76 35 40 45
77 Leu Arg Arg Lys Glu Arg Lys Leu Leu Glu Lys Cys Gly Leu Val Gln
78 50 55 60
79 Ser Leu Thr Ser Ile Thr Leu Phe Ile Ile Pro Thr Val Ala Thr Ala
80 65 70 75 80
81 Val Trp Val Leu Ile His Thr Ser Leu Lys Leu Lys Leu Thr Ala Ser
82 85 90 95
83 Met Ala Phe Ser Met Leu Ala Ser Leu Asn Leu Leu Arg Leu Ser Val
84 100 105 110
85 Phe Phe Val Pro Ile Ala Val Lys Gly Leu Thr Asn Ser Lys Ser Ala
86 115 120 125
87 Val Met Arg Phe Lys Lys Phe Phe Leu Gln Glu Ser Pro Val Phe Tyr
88 130 135 140
89 Val Gln Thr Leu Gln Asp Pro Ser Lys Ala Leu Val Phe Glu Glu Ala
90 145 150 155 160
91 Thr Leu Ser Trp Gln Gln Thr Cys Pro Gly Ile Val Asn Gly Ala Leu
92 165 170 175
93 Glu Leu Glu Arg Asn Gly His Ala Ser Glu Gly Met Thr Arg Pro Arg
94 180 185 190
95 Asp Ala Leu Gly Pro Glu Glu Glu Gly Asn Ser Leu Gly Pro Glu Leu
96 195 200 205
97 His Lys Ile Asn Leu Val Val Ser Lys Gly Met Met Leu Gly Val Cys
98 210 215 220
99 Gly Asn Thr Gly Ser Gly Lys Ser Ser Leu Leu Ser Ala Ile Leu Glu
100 225 230 235 240
101 Glu Met His Leu Leu Glu Gly Ser Val Gly Val Gln Gly Ser Leu Ala
102 245 250 255
103 Tyr Val Pro Gln Ala Trp Ile Val Ser Gly Asn Ile Arg Glu Asn
104 260 265 270
105 Ile Leu Met Gly Gly Ala Tyr Asp Lys Ala Arg Tyr Leu Gln Val Leu
106 275 280 285
107 His Cys Cys Ser Leu Asn Arg Asp Leu Glu Leu Leu Pro Phe Gly Asp

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108      290      295      300
109 Met Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Lys
110 305      310      315      320
111 Gln Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Ile Tyr
112      325      330      335
113 Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His
114      340      345      350
115 Ile Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val
116      355      360      365
117 Leu Val Thr His Gln Leu Gln Tyr Leu Glu Phe Cys Gly Gln Ile Ile
118      370      375      380
119 Leu Leu Glu Asn Gly Lys Ile Cys Glu Asn Gly Thr His Ser Glu Leu
120 385      390      395      400
121 Met Gln Lys Lys Gly Lys Tyr Ala Gln Leu Ile Gln Lys Met His Lys
122      405      410      415
123 Glu Ala Thr Ser Asp Met Leu Gln Asp Thr Ala Lys Ile Ala Glu Lys
124      420      425      430
125 Pro Lys Val Glu Ser Gln Ala Leu Ala Thr Ser Leu Glu Glu Ser Leu
126      435      440      445
127 Asn Gly Asn Ala Val Pro Glu His Gln Leu Thr Gln Glu Glu Glu Met
128      450      455      460
129 Glu Glu Gly Ser Leu Ser Trp Arg Val Tyr His His Tyr Ile Gln Ala
130 465      470      475      480
131 Ala Gly Gly Tyr Met Val Ser Cys Ile Ile Phe Phe Phe Val Val Leu
132      485      490      495
133 Ile Val Phe Leu Thr Ile Phe Ser Phe Trp Trp Leu Ser Tyr Trp Leu
134      500      505      510
135 Glu Gln Gly Ser Gly Thr Asn Ser Ser Arg Glu Ser Asn Gly Thr Met
136      515      520      525
137 Ala Asp Leu Gly Asn Ile Ala Asp Asn Pro Gln Leu Ser Phe Tyr Gln
138      530      535      540
139 Leu Val Tyr Gly Leu Asn Ala Leu Leu Leu Ile Cys Val Gly Val Cys
140 545      550      555      560
141 Ser Ser Gly Ile Phe Thr Lys Val Thr Arg Lys Ala Ser Thr Ala Leu
142      565      570      575
143 His Asn Lys Leu Phe Asn Lys Val Phe Arg Cys Pro Met Ser Phe Phe
144      580      585      590
145 Asp Thr Ile Pro Ile Gly Arg Leu Leu Asn Cys Phe Ala Gly Asp Leu
146      595      600      605
147 Glu Gln Leu Asp Gln Leu Leu Pro Ile Phe Ser Glu Gln Phe Leu Val
148      610      615      620
149 Leu Ser Leu Met Val Ile Ala Val Leu Leu Ile Val Ser Val Leu Ser
150 625      630      635      640
151 Pro Tyr Ile Leu Leu Met Gly Ala Ile Ile Met Val Ile Cys Phe Ile
152      645      650      655
153 Tyr Tyr Met
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 2115
158 <212> TYPE: DNA

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159 <213> ORGANISM: homo sapiens
161 <400> SEQUENCE: 3
162 atgacaagaa tggctgtgaa ggctcagcat cacacatctg aggtcagcga ccagcgcac 60
163 cgtgtgacca gtgaagttct cacttgcat aagctgatta aaatgtacac atgggagaaa 120
164 ccatttgcaa aaatcattga agacctaaga aggaaggaaa ggaagctatt ggagaagtgc 180
165 gggcttgctc agagcctgac aagtataacc ttgttcatca tccccacagt ggccacagcg 240
166 gtctgggttc tcatccacac atccttaaaag ctgaaactca cagcgtcaat ggccttcagc 300
167 atgctggcct ccttgaatct ccttcggctg tcagtgttct ttgtgcctat tgcagtcaaa 360
168 ggtctcacga attccaagtc tgcagtgatg aggttcaaga agtttttcct ccaggagagc 420
169 cctgttttct atgtccagac attacaagac cccagcaaag ctctggctct tgaggaggcc 480
170 acctgtgcat ggcaacagac ctgtcccggg atcgtcaatg gggcactgga gctggagagg 540
171 aacgggcatg cttctgaggg gatgaccagg cctagagatg ccctcgggcc agaggaagaa 600
172 gggaacagcc tggggccaga gttgcacaag atcaacctgg tgggtgtcaa ggggatgatg 660
173 ttaggggtct gcggcaacac ggggagtggt aagagcagcc tgttgtcagc catcctggag 720
174 gagatgact tgcctgaggg ctcggtgggg gtgcaggaa gcctggccta tgtccccag 780
175 caggcctgga tcgtcagcgg gaacatcagg gagaacatcc tcatgggagg cgcataatgac 840
176 aaggcccgat acctccaggt gctccactgc tgctccctga atcgggacct ggaacttctg 900
177 ccctttggag acatgacaga gattggagag cggggcctca acctctctgg ggggcagaaa 960
178 cagaggatca gcctggcccg cgccgtctat tccgaccgtc agatctacct gctggacgac 1020
179 cccctgtctg ctgtggacgc ccacgtgggg aagcacattt ttgaggagtg cattaagaag 1080
180 aactcaggg ggaagacggt cgtcctgggtg acccaccagc tgcagtactt agaattttgt 1140
181 ggccagatca ttttgttgga aaatgggaaa atctgtgaaa atggaactca cagtgaattt 1200
182 atgcagaaaa aggggaaata tgcccaactt atccagaaga tgcacaagga agccacttcg 1260
183 gacatgttgc aggacacagc aaagatagca gagaagccaa aggtagaaag tcaggctctg 1320
184 gccacctccc tggaagagtc tctcaacgga aatgctgtgc cggagcatca gctcacacag 1380
185 gaggaggaga tggaagaagg ctcttgagt tggagggtct accaccata catccaggca 1440
186 cgtggagggt acatggtctc ttgcataatt ttcttctctg tgggtctgat cgtcttctta 1500
187 acgatcttca gcttctggtg gctgagctac tgggtggagc agggctcggg gaccaatagc 1560
188 agccgagaga gcaatggaac catggcagac ctgggcaaca ttgcagacaa tcctcaactg 1620
189 tccttctacc agctggtgta cgggctcaac gccctgctcc tcatctgtgt gggggtctgc 1680
190 tcctcagggg ttttcaccaa ggtcacgagg aaggcatcca cggccctgca caacaagctc 1740
191 ttcaacaagg ttttccgctg ccccatgagt ttctttgaca ccatcccaat aggccggctt 1800
192 ttgaactgct tcgcagggga cttggaacag ctggaccagc tcttgcccat cttttcagag 1860
193 cagttcctgg tcctgtcctt aatggtgatc gccgtcctgt tgattgtcag tgtgctgtct 1920
194 ccatatatcc tgtaaatggg agccataatc atggttattt gcttcattta ttatatgatg 1980
195 ttcaagaagg ccacgtgtgt gttcaagaga ctggagaact atagccggtc tcctttattc 2040
196 tcccacatcc tcaattctct gcaaggcctg agtccatcc atgtctatgg aaaaactgaa 2100
197 gacttcatca gccag 2115
199 <210> SEQ ID NO: 4
200 <211> LENGTH: 705
201 <212> TYPE: PRT
202 <213> ORGANISM: homo sapiens
204 <400> SEQUENCE: 4
205 Met Thr Arg Met Ala Val Lys Ala Gln His His Thr Ser Glu Val Ser
206 1 5 10 15
207 Asp Gln Arg Ile Arg Val Thr Ser Glu Val Leu Thr Cys Ile Lys Leu
208 20 25 30
209 Ile Lys Met Tyr Thr Trp Glu Lys Pro Phe Ala Lys Ile Ile Glu Asp
210 35 40 45

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211 Leu Arg Arg Lys Glu Arg Lys Leu Leu Glu Lys Cys Gly Leu Val Gln
212      50      55      60
213 Ser Leu Thr Ser Ile Thr Leu Phe Ile Ile Pro Thr Val Ala Thr Ala
214 65      70      75      80
215 Val Trp Val Leu Ile His Thr Ser Leu Lys Leu Lys Leu Thr Ala Ser
216      85      90      95
217 Met Ala Phe Ser Met Leu Ala Ser Leu Asn Leu Leu Arg Leu Ser Val
218      100      105      110
219 Phe Phe Val Pro Ile Ala Val Lys Gly Leu Thr Asn Ser Lys Ser Ala
220      115      120      125
221 Val Met Arg Phe Lys Lys Phe Phe Leu Gln Glu Ser Pro Val Phe Tyr
222      130      135      140
223 Val Gln Thr Leu Gln Asp Pro Ser Lys Ala Leu Val Phe Glu Glu Ala
224 145      150      155      160
225 Thr Leu Ser Trp Gln Gln Thr Cys Pro Gly Ile Val Asn Gly Ala Leu
226      165      170      175
227 Glu Leu Glu Arg Asn Gly His Ala Ser Glu Gly Met Thr Arg Pro Arg
228      180      185      190
229 Asp Ala Leu Gly Pro Glu Glu Glu Gly Asn Ser Leu Gly Pro Glu Leu
230      195      200      205
231 His Lys Ile Asn Leu Val Val Ser Lys Gly Met Met Leu Gly Val Cys
232      210      215      220
233 Gly Asn Thr Gly Ser Gly Lys Ser Ser Leu Leu Ser Ala Ile Leu Glu
234 225      230      235      240
235 Glu Met His Leu Leu Glu Gly Ser Val Gly Val Gln Gly Ser Leu Ala
236      245      250      255
237 Tyr Val Pro Gln Gln Ala Trp Ile Val Ser Gly Asn Ile Arg Glu Asn
238      260      265      270
239 Ile Leu Met Gly Gly Ala Tyr Asp Lys Ala Arg Tyr Leu Gln Val Leu
240      275      280      285
241 His Cys Cys Ser Leu Asn Arg Asp Leu Glu Leu Leu Pro Phe Gly Asp
242      290      295      300
243 Met Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Lys
244 305      310      315      320
245 Gln Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Ile Tyr
246      325      330      335
247 Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His
248      340      345      350
249 Ile Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val
250      355      360      365
251 Leu Val Thr His Gln Leu Gln Tyr Leu Glu Phe Cys Gly Gln Ile Ile
252      370      375      380
253 Leu Leu Glu Asn Gly Lys Ile Cys Glu Asn Gly Thr His Ser Glu Leu
254 385      390      395      400
255 Met Gln Lys Lys Gly Lys Tyr Ala Gln Leu Ile Gln Lys Met His Lys
256      405      410      415
257 Glu Ala Thr Ser Asp Met Leu Gln Asp Thr Ala Lys Ile Ala Glu Lys
258      420      425      430
259 Pro Lys Val Glu Ser Gln Ala Leu Ala Thr Ser Leu Glu Glu Ser Leu

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VERIFICATION SUMMARY

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Input Set : A:\lex81usa SEQLIST.TXT

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L:18 M:270 C: Current Application Number differs, Replaced Current Application No

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date